

1127

1633

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RAW SEQUENCE LISTING DATE: 05/04/2000
 PATENT APPLICATION: US/08/900,220B TIME: 13:10:49

Input Set : A:\ONV-044.01.txt
 Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw

4 (1) GENERAL INFORMATION:
 C--> 6 (i) APPLICANT: Miao, Ningning
 7 Wang, Monica
 8 Mahanthappa, Nagesh K.
 9 Jin, Ping
 10 Wang Pang, Kevin
 12 (ii) TITLE OF INVENTION: Method of Treating Dopaminergic and
 13 GABA-nergic Disorders
 15 (iii) NUMBER OF SEQUENCES: 22
 17 (iv) CORRESPONDENCE ADDRESS:
 18 (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 19 (B) STREET: ONE POST OFFICE SQUARE
 20 (C) CITY: Boston
 21 (D) STATE: MA
 22 (E) COUNTRY: USA
 23 (F) ZIP: 02109
 25 (v) COMPUTER READABLE FORM:
 26 (A) MEDIUM TYPE: Floppy disk
 27 (B) COMPUTER: IBM PC compatible
 28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 29 (D) SOFTWARE: ASCII (text)
 C--> 31 (vi) CURRENT APPLICATION DATA:
 C--> 32 (A) APPLICATION NUMBER: US/08/900,220B
 C--> 33 (B) FILING DATE: 24-Jul-1997
 34 (C) CLASSIFICATION:
 36 (viii) ATTORNEY/AGENT INFORMATION:
 37 (A) NAME: Vincent, Matthew P.
 38 (B) REGISTRATION NUMBER: 36,709
 39 (C) REFERENCE/DOCKET NUMBER: ONV-044.01
 41 (ix) TELECOMMUNICATION INFORMATION:
 42 (A) TELEPHONE: (617) 832-1000
 43 (B) TELEFAX: (617) 832-7000
 46 (2) INFORMATION FOR SEQ ID NO: 1:
 47 (i) SEQUENCE CHARACTERISTICS:
 48 (A) LENGTH: 1277 base pairs
 49 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: both
 51 (D) TOPOLOGY: linear
 53 (ii) MOLECULE TYPE: cDNA
 55 (ix) FEATURE:
 56 (A) NAME/KEY: CDS
 57 (B) LOCATION: 1..1275
 59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 61 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC 48
 62 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
 63 1 5 10 15
 65 TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC 96

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66 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly		
67 20 25	30	
69 ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG		144
70 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys		
71 35 40	45	
73 CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA		192
74 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg		
75 50 55	60	
77 TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC		240
78 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr		
79 65 70 75	80	
81 CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA		288
82 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly		
83 85 90	95	
85 GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG		336
86 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu		
87 100 105	110	
89 GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC		384
90 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr		
91 115 120	125	
93 GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC		432
94 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr		
95 130 135	140	
97 GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG		480
98 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys		
99 145 150	155	160
101 TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC		528
102 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val		
103 165 170	175	
105 TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC		576
106 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn		
107 180 185	190	
109 TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG		624
110 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val		
111 195 200	205	
113 CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG		672
114 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly		
115 210 215	220	
117 GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC		720
118 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp		
119 225 230	235	240
121 TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC		768
122 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr		
123 245 250	255	
125 GTC ATC GAG ACG CGG CAG CCC CGG GCC CGG CTG CTA CTG ACG GCG GCC		816
126 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Thr Ala Ala		
127 260 265	270	
129 CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGG		
130 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly		864

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131	275	280	285	
133	TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA			912
134	Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln			
135	290	295	300	
137	CGT GTC TAT GTG CTG GGC GAG GGG CAG CAG CTG CTG CCG GCG TCT			960
138	Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser			
139	305	310	315	320
141	GTC CAC AGC GTC TCA TTG CGG GAG GAG GCG TCC GGA GCC TAC GCC CCA			1008
142	Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro			
143	325	330	335	
145	CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC			1056
146	Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys			
147	340	345	350	
149	TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA			1104
150	Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro			
151	355	360	365	
153	TTC CGC TTG GCT CAG GGG CTG CTG GCC CTC TGC CCA GAT GGG GCC			1152
154	Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala			
155	370	375	380	
157	ATC CCT ACT GCC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG			1200
158	Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg			
159	385	390	395	400
160	CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT			1248
161	Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His			
162	405	410	415	
164	CCG CTG GGC ATG GTG GCA CCG GCC AGC TG			1277
165	Pro Leu Gly Met Val Ala Pro Ala Ser			
166	420	425		
169	(2) INFORMATION FOR SEQ ID NO: 2:			
171	(i) SEQUENCE CHARACTERISTICS:			
172	(A) LENGTH: 1190 base pairs			
173	(B) TYPE: nucleic acid			
174	(C) STRANDEDNESS: both			
175	(D) TOPOLOGY: linear			
177	(ii) MOLECULE TYPE: cDNA			
179	(ix) FEATURE:			
180	(A) NAME/KEY: CDS			
181	(B) LOCATION: 1..1191			
183	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
185	ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG			48
186	Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu			
187	1 5 10 15			
189	GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG			96
190	Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg			
191	20 25 30			
193	CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT			144
194	Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe			
195	35 40 45			
197	GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG			192

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Input Set : A:\ONV-044.01.txt
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198	Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu	
199				50				55					60				
201	GGG	AGG	GTA	ACA	AGG	GGG	TCG	GAG	CGC	TTC	CGG	GAC	CTC	GTA	CCC	AAC	
202	Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn	
203	65				70					75			80				
205	TAC	AAC	CCC	GAC	ATA	ATC	TTC	AAG	GAT	GAG	GAG	AAC	AGC	GGC	GCA	GAC	
206	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp	
207				85					90			95					
209	CGC	CTG	ATG	ACA	GAG	CGT	TGC	AAA	GAG	CGG	GTG	AAC	GCT	CTA	GCC	ATC	
210	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile	
211				100				105				110					
213	GCG	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTA	CGC	CTA	CGT	GTG	ACT	GAA	GGC	
214	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
215				115				120			125						
217	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCA	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	
218	Trp	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
219				130				135			140						
221	CGT	GCC	TTG	GAC	ATC	ACC	ACG	TCT	GAC	CGT	GAC	CGT	AAT	AAG	TAT	GGT	
222	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
223	145				150				155			160					
225	TTG	TTG	GCG	CGC	CTA	GCT	GTG	GAA	GCC	GGA	TTC	GAC	TGG	GTC	TAC	TAC	
226	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
227				165				170			175						
229	GAG	TCC	CGC	AAC	CAC	ATC	CAC	GTA	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	
230	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
231				180				185			190						
233	GCG	GTC	CGA	GCC	GGG	GGC	TGC	TTT	CCG	GGA	AAT	GCC	ACG	GTG	CGC	TTG	
234	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
235				195				200			205						
237	CGG	AGC	GCG	GAA	CGG	AAG	GGG	CTG	AGG	GAA	CTA	CAT	CGT	GGT	GAC	TGG	
238	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
239				210				215			220						
241	GTA	CTG	GCC	GCT	GAT	GCA	GCG	GGC	CGA	GTG	GTA	CCC	ACG	CCA	GTG	CTG	
242	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
243	225				230				235			240					
245	CTC	TTC	CTG	GAC	CGG	GAT	CTG	CAG	CGC	CGC	GCC	TCG	TTC	GTG	GCT	GTG	
246	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
247				245				250			255						
249	GAG	ACC	GAG	CGG	CCT	CCG	CGC	AAA	CTG	TTG	CTC	ACA	CCC	TGG	CAT	CTG	
250	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Ieu	Ieu	Ieu	Thr	Pro	Trp	His	Ieu	
251				260				265			270						
253	GTG	TTC	GCT	GCT	CGC	GGG	CCA	GCG	CCT	GCT	CCA	GGT	GAC	TTT	GCA	CCG	
254	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
255				275				280			285						
257	GTG	TTC	GCG	CGC	CGC	TTA	CGT	GCT	GGC	GAC	TCG	GTG	CTG	GCT	CCC	GGC	
258	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Ieu	Ala	Pro	Gly	
259				290				295			300						
261	GGG	GAC	GCG	CTC	CAG	CCG	GCG	CGC	GTA	GCC	CGC	GTG	GCG	CGC	GAG	GAA	
262	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu	

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 Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw

263	305	310	315	320	
265	GCC GTG GGC GTG	TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC			1008
266	Ala Val Gly Val	Phe Ala Pro Leu Thr Ala His G _{ly} Thr Leu Leu Val			
267		325	330	335	
269	AAC GAC GTC CTC	GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG			1056
270	Asn Asp Val Leu Ala Ser Cys Tyr	Ala Val Leu Glu Ser His Gln Trp			
271		340	345	350	
273	GCC CAC CGC GCC	TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT			1104
274	Ala His Arg Ala	Phe Ala Pro Leu Arg Leu Leu His Ala Leu G _{ly} Ala			
275		355	360	365	
277	CTG CTC CCT GGG GGT	GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT			1152
278	Leu Leu Pro Gly	Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser			
279		370	375	380	
281	CGC CTC CTT TAC CGC	TTG GCC GAG GAG TTA ATG GGC TG			1190
282	Arg Leu Leu Tyr	Arg Leu Ala Glu Glu Leu Met Gly			
283	385		390	395	
286	(2) INFORMATION FOR SEQ ID NO: 3:				
288	(i) SEQUENCE CHARACTERISTICS:				
289	(A) LENGTH: 1281 base pairs				
290	(B) TYPE: nucleic acid				
291	(C) STRANDEDNESS: both				
292	(D) TOPOLOGY: linear				
294	(ii) MOLECULE TYPE: cDNA				
297	(ix) FEATURE:				
298	(A) NAME/KEY: CDS				
299	(B) LOCATION: 1..1233				
301	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:				
303	ATG TCT CCC GCC	TGG CTC CCG CCC CGA CTG CGG TTC TGT CTG TTC CTG			48
304	Met Ser Pro Ala Trp	Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu			
305	1	5	10	15	
307	CTG CTG CTG CTT	CTG GTG CCG GCG GCG CGG GGC TGC GGG CCG GGC CGG			96
308	Leu Leu Leu Leu Val	Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg			
309		20	25	30	
311	GTG GTG GGC AGC	CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC			144
312	Val Val Gly Ser	Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala			
313		35	40	45	
315	TAC AAG CAG TTC	AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC			192
316	Tyr Lys Gln Phe	Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser			
317		50	55	60	
319	GGG CGC TAC GAA	GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG			240
320	Gly Arg Tyr Glu	Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu			
321		65	70	75	80
323	CTC ACC CCC AAC	TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC			288
324	Leu Thr Pro Asn	Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn			
325		85	90	95	
327	ACG GGT GCC GAC	CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC			336
328	Thr Gly Ala Asp	Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn			
329		100	105	110	
331	TCA CTG GCC ATC	TCT GTC ATG AAC CAG TGG CCT GGT GTG AAA CTG CGG			384

VERIFICATION SUMMARY DATE: 05/04/2000
PATENT APPLICATION: US/08/900,220B TIME: 13:10:50

Input Set : A:\ONV-044.01.txt
Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw

L:6 M:220 C: Keyword misspelled, [(i) APPLICANT:]
L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22